

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/126,016DATE: 11/03/97
TIME: 16:58:22

INPUT SET: S21354.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

SEQUENCE LISTING

1
2
3 (1) General Information:
4
5 (i) APPLICANT: WALLACH, DAVID
6 NOPHAR, YARON
7 KEMPER, OLIVER
8 ENGELMANN, HARTMUT
9 BRAKEBUSCH, CORD
10 ADERKA, DAN
11
12 (ii) TITLE OF INVENTION: EXPRESSION OF THE RECOMBINANT TUMOR
13 NECROSIS FACTOR BINDING PROTEIN I (TBP-I)
14
15 (iii) NUMBER OF SEQUENCES: 26
16
17 (iv) CORRESPONDENCE ADDRESS:
18 (A) ADDRESSEE: Browdy and Neimark
19 (B) STREET: 419 Seventh Street, N.W., Suite 300
20 (C) CITY: Washington
21 (D) STATE: DC
22 (E) COUNTRY: USA
23 (F) ZIP: 20004
24
25 (v) COMPUTER READABLE FORM:
26 (A) MEDIUM TYPE: Floppy disk
27 (B) COMPUTER: IBM PC compatible
28 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
29 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
30
31 (vi) CURRENT APPLICATION DATA:
32 (A) APPLICATION NUMBER: 08/126,016
33 (B) FILING DATE: 24-SEP-1993
34 (C) CLASSIFICATION: 435
35
36 (vii) PRIOR APPLICATION DATA:
37 (A) APPLICATION NUMBER: US 07/625668
38 (B) FILING DATE: 13-DEC-1990
39
40 (viii) ATTORNEY/AGENT INFORMATION:
41 (A) NAME: BROWDY, ROGER L
42 (B) REGISTRATION NUMBER: 25,618
43 (C) REFERENCE/DOCKET NUMBER: WALLACH4
44
45 (ix) TELECOMMUNICATION INFORMATION:
46 (A) TELEPHONE: 202-628-5197

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47 (B) TELEFAX: 202-737-3528
48 (C) TELEX: 248633
49
50

51 (2) INFORMATION FOR SEQ ID NO:1:
52

53 (i) SEQUENCE CHARACTERISTICS:
54 (A) LENGTH: 2175 base pairs
55 (B) TYPE: nucleic acid
56 (C) STRANDEDNESS: single
57 (D) TOPOLOGY: linear
58

59 (ii) MOLECULE TYPE: cDNA
6061 (ix) FEATURE:
62

63 (A) NAME/KEY: CDS
64 (B) LOCATION: 256..1620
65

66 (ix) FEATURE:
67

68 (A) NAME/KEY: mat_peptide
69 (B) LOCATION: 319..1620
70

71 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
72

73	CGGCCCAGTG ATCTTGAACC CCAAAGGCCA GAACTGGAGC CTCAGTCCAG AGAATTCTGA	60
74		
75	GAAAAATTAAG GCAGAGAGGA GGGGAGAGAT CACTGGGACC AGGCCGTGAT CTCTATGCCC	120
76		
77	GAGTCTCAAC CCTCAACTGT CACCCCAAGG CACTTGGGAC GTCCTGGACA GACCGAGTCC	180
78		
79	CGGGAAGCCC CAGCACTGCC GCTGCCACAC TGCCCTGAGC CCAAATGGGG GAGTGAGAGG	240
80		
81	CCATAGCTGT CTGGC ATG GGC CTC TCC ACC GTG CCT GAC CTG CTG CTG CCG	291
82	Met Gly Leu Ser Thr Val Pro Asp Leu Leu Leu Pro	
83	-21 -20 -15 -10	
84		
85	CTG GTG CTC CTG GAG CTG TTG GTG GGA ATA TAC CCC TCA GGG GTT ATT	339
86	Leu Val Leu Leu Glu Leu Leu Val Gly Ile Tyr Pro Ser Gly Val Ile	
87	-5 1 5	
88		
89	GGA CTG GTC CCT CAC CTA GGG GAC AGG GAG AAG AGA GAT AGT GTG TGT	387
90	Gly Leu Val Pro His Leu Gly Asp Arg Glu Lys Arg Asp Ser Val Cys	
91	10 15 20	
92		
93	CCC CAA GGA AAA GAT ATC CAC CCT CAA AAT AAT TCG ATT TGC TGT ACC	435
94	Pro Gln Gly Lys Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr	
95	25 30 35	
96		
97	AAG TGC CAC AAA GGA ACC TAC TTG TAC AAT GAC TGT CCA GGC CCG GGG	483
98	Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly	
99	40 45 50 55	

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100																	
101	CAG	GAT	ACG	GAC	TGC	AGG	GAG	TGT	GAG	AGC	GGC	TCC	TTC	ACC	GCT	TCA	531
102	Gln	Asp	Thr	Asp	Cys	Arg	Glu	Cys	Glu	Ser	Gly	Ser	Phe	Thr	Ala	Ser	
103					60					65					70		
104																	
105	GAA	AAC	CAC	CTC	AGA	CAC	TGC	CTC	AGC	TGC	TCC	AAA	TGC	CGA	AAG	GAA	579
106	Glu	Asn	His	Leu	Arg	His	Cys	Leu	Ser	Cys	Ser	Lys	Cys	Arg	Lys	Glu	
107				75					80					85			
108																	
109	ATG	GGT	CAG	GTG	GAG	ATC	TCT	TCT	TGC	ACA	GTG	GAC	CGG	GAC	ACC	GTG	627
110	Met	Gly	Gln	Val	Glu	Ile	Ser	Ser	Cys	Thr	Val	Asp	Arg	Asp	Thr	Val	
111			90					95					100				
112																	
113	TGT	GGC	TGC	AGG	AAG	AAC	CAG	TAC	CGG	CAT	TAT	TGG	AGT	GAA	AAC	CTT	675
114	Cys	Gly	Cys	Arg	Lys	Asn	Gln	Tyr	Arg	His	Tyr	Trp	Ser	Glu	Asn	Leu	
115		105					110					115					
116																	
117	TTC	CAG	TGC	TTC	AAT	TGC	AGC	CTC	TGC	CTC	AAT	GGG	ACC	GTG	CAC	CTC	723
118	Phe	Gln	Cys	Phe	Asn	Cys	Ser	Leu	Cys	Leu	Asn	Gly	Thr	Val	His	Leu	
119	120					125					130					135	
120																	
121	TCC	TGC	CAG	GAG	AAA	CAG	AAC	ACC	GTG	TGC	ACC	TGC	CAT	GCA	GGT	TTC	771
122	Ser	Cys	Gln	Glu	Lys	Gln	Asn	Thr	Val	Cys	Thr	Cys	His	Ala	Gly	Phe	
123					140					145					150		
124																	
125	TTT	CTA	AGA	GAA	AAC	GAG	TGT	GTC	TCC	TGT	AGT	AAC	TGT	AAG	AAA	AGC	819
126	Phe	Leu	Arg	Glu	Asn	Glu	Cys	Val	Ser	Cys	Ser	Asn	Cys	Lys	Lys	Ser	
127				155					160					165			
128																	
129	CTG	GAG	TGC	ACG	AAG	TTG	TGC	CTA	CCC	CAG	ATT	GAG	AAT	GTT	AAG	GGC	867
130	Leu	Glu	Cys	Thr	Lys	Leu	Cys	Leu	Pro	Gln	Ile	Glu	Asn	Val	Lys	Gly	
131			170					175					180				
132																	
133	ACT	GAG	GAC	TCA	GGC	ACC	ACA	GTG	CTG	TTG	CCC	CTG	GTC	ATT	TTC	TTT	915
134	Thr	Glu	Asp	Ser	Gly	Thr	Thr	Val	Leu	Leu	Pro	Leu	Val	Ile	Phe	Phe	
135		185					190					195					
136																	
137	GGT	CTT	TGC	CTT	TTA	TCC	CTC	CTC	TTC	ATT	GGT	TTA	ATG	TAT	CGC	TAC	963
138	Gly	Leu	Cys	Leu	Leu	Ser	Leu	Leu	Phe	Ile	Gly	Leu	Met	Tyr	Arg	Tyr	
139	200					205											

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153	TTC AGT CCC GTG CCC AGT TCC ACC TTC ACC TCC AGC TCC ACC TAT ACC	1155
154	Phe Ser Pro Val Pro Ser Ser Thr Phe Thr Ser Ser Ser Thr Tyr Thr	
155	265 270 275	
156		
157	CCC GGT GAC TGT CCC AAC TTT GCG GCT CCC CGC AGA GAG GTG GCA CCA	1203
158	Pro Gly Asp Cys Pro Asn Phe Ala Ala Pro Arg Arg Glu Val Ala Pro	
159	280 285 290 295	
160		
161	CCC TAT CAG GGG GCT GAC CCC ATC CTT GCG ACA GCC CTC GCC TCC GAC	1251
162	Pro Tyr Gln Gly Ala Asp Pro Ile Leu Ala Thr Ala Leu Ala Ser Asp	
163	300 305 310	
164		
165	CCC ATC CCC AAC CCC CTT CAG AAG TGG GAG GAC AGC GCC CAC AAG CCA	1299
166	Pro Ile Pro Asn Pro Leu Gln Lys Trp Glu Asp Ser Ala His Lys Pro	
167	315 320 325	
168		
169	CAG AGC CTA GAC ACT GAT GAC CCC GCG ACG CTG TAC GCC GTG GTG GAG	1347
170	Gln Ser Leu Asp Thr Asp Asp Pro Ala Thr Leu Tyr Ala Val Val Glu	
171	330 335 340	
172		
173	AAC GTG CCC CCG TTG CGC TGG AAG GAA TTC GTG CGG CGC CTA GGG CTG	1395
174	Asn Val Pro Pro Leu Arg Trp Lys Glu Phe Val Arg Arg Leu Gly Leu	
175	345 350 355	
176		
177	AGC GAC CAC GAG ATC GAT CGG CTG GAG CTG CAG AAC GGG CGC TGC CTG	1443
178	Ser Asp His Glu Ile Asp Arg Leu Glu Leu Gln Asn Gly Arg Cys Leu	
179	360 365 370 375	
180		
181	CGC GAG GCG CAA TAC AGC ATG CTG GCG ACC TGG AGG CGG CGC ACG CCG	1491
182	Arg Glu Ala Gln Tyr Ser Met Leu Ala Thr Trp Arg Arg Arg Thr Pro	
183	380 385 390	
184		
185	CGG CGC GAG GCC ACG CTG GAG CTG CTG GGA CGC GTG CTC CGC GAC ATG	1539
186	Arg Arg Glu Ala Thr Leu Glu Leu Gly Arg Val Leu Arg Asp Met	
187	395 400 405	
188		
189	GAC CTG CTG GGC TGC CTG GAG GAC ATC GAG GAG GCG CTT TGC GGC CCC	1587
190	Asp Leu Leu Gly Cys Leu Glu Asp Ile Glu Glu Ala Leu Cys Gly Pro	
191	410 415 420	
192		
193	GCC GCC CTC CCG CCC GCG CCC AGT CTT CTC AGA TGAGGCTGCG CCCTGCGGGC	1640
194	Ala Ala Leu Pro Pro Ala Pro Ser Leu Leu Arg	
195	425 430	
196		
197	AGCTCTAAGG ACCGTCCTGC GAGATCGCCT TCCAACCCCA CTTTTTTCTG GAAAGGAGGG	1700
198		
199	GTCTGTCAGG GGCAAGCAGG AGCTAGCAGC CGCCTACTTG GTGCTAACCC CTGGATGTAC	1760
200		
201	ATAGCTTTTC TCAGCTGCCT GCGCGCCGCC GACAGTCAGC GCTGTGCCCG CGGAGAGAGG	1820
202		
203	TGCGCCGTGG GCTCAAGAGC CTGAGTGGGT GGTTCGCGAG GATGAGGAC GCTATGCCTC	1880
204		
205	ATGCCCGTTT TGGGTGTCCT CACCAGCAAG GCTGCTCGGG GGCCCTGCT TCGTCCCTGA	1940

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206
207 GCCTTTTTC A CAGTGCATAA GCAGTTTTTT TTGTTTTTGT TTTGTTTTGT TTTGTTTTTA 2000
208
209 AATCAATCAT GTTACACTAA TAGAACTTG GCACTCCTGT GCCCTCTGCC TGGACAAGCA 2060
210
211 CATAGCAAGC TGAAGTGTCC TAAGGCAGGG GCGAGCACGG AACAATGGGG CCTTCAGCTG 2120
212
213 GAGCTGTGGA CTTTTGTACA TACACTAAAA TTCTGAAGTT AAAAAAAAAA AAAAA 2175
214
215

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 455 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

226
227 Met Gly Leu Ser Thr Val Pro Asp Leu Leu Leu Pro Leu Val Leu Leu
228 -21 -20 -15 -10
229
230 Glu Leu Leu Val Gly Ile Tyr Pro Ser Gly Val Ile Gly Leu Val Pro
231 -5 1 5 10
232
233 His Leu Gly Asp Arg Glu Lys Arg Asp Ser Val Cys Pro Gln Gly Lys
234 15 20 25
235
236 Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr Lys Cys His Lys
237 30 35 40
238
239 Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Gln Asp Thr Asp
240 45 50 55
241
242 Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu Asn His Leu
243 60 65 70 75
244
245 Arg His Cys Leu Ser Cys Ser Lys Cys Arg Lys Glu Met Gly Gln Val
246 80 85 90
247
248 Glu Ile Ser Ser Cys Thr Val Asp Arg Asp Thr Val Cys Gly Cys Arg
249 95 100 105
250
251 Lys Asn Gln Tyr Arg His Tyr Trp Ser Glu Asn Leu Phe Gln Cys Phe
252 110 115 120
253
254 Asn Cys Ser Leu Cys Leu Asn Gly Thr Val His Leu Ser Cys Gln Glu
255 125 130 135
256
257 Lys Gln Asn Thr Val Cys Thr Cys His Ala Gly Phe Phe Leu Arg Glu
258 140 145 150 155

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SEQUENCE VERIFICATION REPORT
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